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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=9; day=16; hr=8; min=29; sec=11; ms=981;]

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Reviewer Comments:

<110> Center for Genetic Engineering and Biotechnology

<120> Antiangiogenic active immunotherapies

<130> 976-19 PCT/US/RCE

<140> 10/511,384

<141> 2004-10-15

<150> CU 2002/0076

<151> 2002-04-15

<160> 229

Numeric identifier <160> must reflect the total number of sequences in the sequence listing. There are only 226 sequences in this sequence listing but, <160> states there are 229. Please make all necessary changes

<210> 129

<212> PRT

<213> Artificial Sequence

<220>

<223> VEGFR-1 derived peptides

<400> 129

Lys Leu Leu Arg Gly His Thr Leu Val

Numeric identifier "<211> Length" is mandatory for each SEQ ID number.

Application No: 10511384 Version No: 3.0

Input Set:

Output Set:

Started: 2008-08-12 14:55:48.277
Finished: 2008-08-12 14:55:50.653
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 376 ms
Total Warnings: 218
Total Errors: 3
No. of SeqIDs Defined: 229
Actual SeqID Count: 226

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)

Input Set:

Output Set:

Started: 2008-08-12 14:55:48.277
Finished: 2008-08-12 14:55:50.653
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 376 ms
Total Warnings: 218
Total Errors: 3
No. of SeqIDs Defined: 229
Actual SeqID Count: 226

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 249	Order Sequence Error <210> -> <212>; Expected Mandatory Tag: <211> in SEQID (129)
E 252	Calc# of Seq. differs from actual; 229 seqIds defined; count=226
E 250	Structural Validation Error; Sequence listing may not be indexable

SEQUENCE LISTING

<110> Center for Genetic Engineering and Biotechnology

<120> Antiangiogenic active immunotherapies

<130> 976-19 PCT/US/RCE

<140> 10/511,384

<141> 2004-10-15

<150> CU 2002/0076

<151> 2002-04-15

<160> 229

<170> PatentIn version 3.4

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<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 1

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21

<210> 2

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 2

gaattcaccg cctcggcttg tc

22

<210> 3

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 3

tggatccatg aactttctgc t

21

<210> 4

<211> 30

<212> DNA

<213> Artificial Sequence

<220>
<223> primer

<400> 4
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<210> 5
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 5
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<210> 6
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 6
gaattcacccg cctcggttg tc

22

<210> 7
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 7
tggatccatg aactttctgc t

21

<210> 8
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 8
gaattcacccg cctcggttg tc

22

<210> 9
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<220>
<223> primer

<400> 9
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<210> 10
<211> 25
<212> DNA
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<220>
<223> primer

<400> 10
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<210> 11
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<212> DNA
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<220>
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<210> 12
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<212> DNA
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<400> 12
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<210> 13
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<220>
<223> primer

<400> 13

gaagatctgt ataaggactt c

21

<210> 14
<211> 19
<212> DNA
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<220>
<223> primer

<400> 14
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19

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<220>
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22

<210> 16
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<400> 16
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20

<210> 17
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<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 17
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21

<210> 18
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

<223> primer

<400> 18

tagcggccgc ttaaacagg

19

<210> 19

<211> 147

<212> PRT

<213> Homo Sapiens

<400> 147

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Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65 70 75 80

Met Arg Cys Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Glu Ile Glu Pro Glu
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
130 135 140

Pro Arg Arg

145

<210> 20

<211> 444

<212> DNA

<213> Homo Sapiens

<400> 20

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gtgaagttca tggatgtcta tcagcgccagc tactgccatc caatcgagac cctgggtggac 180

atcttccagg agtacctga tgagatcgag tacatttca agccatcctg tgtgcccctg 240
atgcgatgcg ggggctgctg caatgacgag ggcctggagt gtgtgccac tgaggagtcc 300
aacatcacca tgcagattat gcggatcaa cctcaccaag gccagcacat aggagagatg 360
agcttcctac agcacaacaa atgtaatgc agaccaaaga aagatagagc aagacaagaa 420
aaatgtgaca agccgaggcg gtga 444

<210> 21
<211> 147
<212> PRT
<213> Homo Sapiens

<400> 147

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Ala Ile Ala Pro Ala
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
130 135 140

Pro Arg Arg
145

<210> 22
<211> 444
<212> DNA
<213> Homo Sapiens

<400> 22
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gccaagtggc cccaggctgc acccatggca gaaggaggag ggcagaatca tcacgaagtg 120
gtgaagttca tggatgtcta tcagcgccgc tactgccatc caatcgagac cctggtggac 180
atcttcagg agtaccctga tgagatcgag tacatcttca agccatcctg tgtgcccctg 240
atgcgatgctg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc 300
aacatcacca tgcagattat ggcaatcgca cctgcacaag gccagcacat aggagagatg 360
agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagac aagacaagaa 420
aatgtgaca agccgaggcg gtaa 444

<210> 23
<211> 314
<212> PRT
<213> Homo Sapiens

<400> 314

Met Glu Ser Lys Val Leu Leu Ala Val Ala Leu Trp Leu Cys Val Glu
1 5 10 15

Thr Arg Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro
20 25 30

Arg Leu Ser Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr
35 40 45

Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro
50 55 60

Asn Asn Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser
65 70 75 80

Asp Gly Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn
85 90 95

Asp Thr Gly Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser
100 105 110

Val Ile Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser
115 120 125

Val Ser Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys
130 135 140

Thr Val Val Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser
145 150 155 160

Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg
165 170 175

Ile Ser Trp Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile

180	185	190
Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Ser		
195	200	205
Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr		
210	215	220
Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu		
225	230	235
240		
Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile		
245	250	255
Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu		
260	265	270
Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe		
275	280	285
Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu		
290	295	300
Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met		
305	310	

<210> 24
 <211> 943
 <212> DNA
 <213> Homo Sapiens

<400> 24

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cttacaattt aggctaatac aactcttcaa attacttgca gggcacagag ggacttggac	180
tggctttggc ccaataatca gagtggcagt gagcaaaggg tggaggtgac tgagtgcac	240
gatggcctct tctgttaagac actcacaatt ccaaaagtga tcggaaatga cactggagcc	300
tacaagtgtct tctaccggga aactgacttg gcctcggtca tttatgtcta tggtaagat	360
tacagatctc catttattgc ttctgttagt gaccaacatg gagtcgtgta cattactgag	420
aacaaaaaaca aaactgtggt gattccatgt ctgggtcca tttcaaattct caacgtgtca	480
ctttgtgcaa gataccaga aaagagatt gttcctgatg gtaacagaat ttccctggac	540
agcaagaagg gctttactat tcccagctac atgatcagct atgctggcat ggtttctgt	600
gaagcaaaaa ttaatgtga aagttaccag tctattatgt acatagttgt cggtgttaggg	660
tataggattt atgatgtggt tctgagtccg tctcatggaa ttgaactatc tggatggagaa	720

aagcttgtct taaattgtac agcaagaact gaactaaatg tggggattga cttcaactgg 780
gaataccctt ctgcgaagca tcagcataag aaacttgtaa accgagacct aaaaaccag 840
tctgggagtg agatgaagaa attttgagc acctaacta tagatggtgt aaccggagt 900
gaccaaggat tgtacacctg tgcatcc agtgggctga tga 943

<210> 25
<211> 611
<212> PRT
<213> Homo sapiens

<400> 611

Ala Lys Val Glu Ala Phe Phe Ile Ile Glu Gly Ala Gln Glu Lys Thr
1 5 10 15

Asn Leu Glu Ile Ile Ile Leu Val Gly Thr Ala Val Ile Ala Met Phe
20 25 30

Phe Trp Leu Leu Leu Val Ile Ile Leu Arg Thr Val Lys Arg Ala Asn
35 40 45

Gly Gly Glu Leu Lys Thr Gly Tyr Leu Ser Ile Val Met Asp Pro Asp
50 55 60

Glu Leu Pro Leu Asp Glu His Cys Glu Arg Leu Pro Tyr Asp Ala Ser
65 70 75 80

Lys Trp Glu Phe Pro Arg Asp Arg Leu Lys Leu Gly Lys Pro Leu Gly
85 90 95

Arg Gly Ala Phe Gly Gln Val Ile Glu Ala Asp Ala Phe Gly Ile Asp
100 105 110

Lys Thr Ala Thr Cys Arg Thr Val Ala Val Lys Met Leu Lys Glu Gly
115 120 125

Ala Thr His Ser Glu His Arg Ala Leu Met Ser Glu Leu Lys Ile Leu
130 135 140

Ile His Ile Gly His His Leu Asn Val Val Asn Leu Leu Gly Ala Cys
145 150 155 160

Thr Lys Pro Gly Gly Pro Leu Met Val Ile Val Glu Phe Cys Lys Phe
165 170 175

Gly Asn Leu Ser Thr Tyr Leu Arg Ser Lys Arg Asn Glu Phe Val Pro
180 185 190

Tyr Lys Thr Lys Gly Ala Arg Phe Arg Gln Gly Lys Asp Tyr Val Gly
195 200 205

Ala Ile Pro Val Asp Leu Lys Arg Arg Leu Asp Ser Ile Thr Ser Ser
210 215 220

Gln Ser Ser Ala Ser Ser Gly Phe Val Glu Glu Lys Ser Leu Ser Asp
225 230 235 240

Val Glu Glu Glu Ala Pro Glu Asp Leu Tyr Lys Asp Phe Leu Thr
245 250 255

Leu Glu His Leu Ile Cys Tyr Ser Phe Gln Val Ala Lys Gly Met Glu
260 265 270

Phe Leu Ala Ser Arg Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn
275 280 285

Ile Leu Leu Ser Glu Lys Asn Val Val Lys Ile Cys Asp Phe Gly Leu
290 295 300

Ala Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly Asp Ala
305 310 315 320

Arg Leu Pro Leu Lys Trp Met Ala Pro Glu Thr Ile Phe Asp Arg Val
325 330 335

Tyr Thr Ile Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu
340 345 350

Ile Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Lys Ile Asp Glu
355 360 365

Glu Phe Cys Arg Arg Leu Lys Glu Gly Thr Arg Met Arg Ala Pro Asp
370 375 380

Tyr Thr Thr Pro Glu Met Tyr Gln Thr Met Leu Asp Cys Trp His Gly

385

390

395

400

Glu Pro Ser Gln Arg Pro Thr Phe Ser Glu Leu Val Glu His Leu Gly
405 410 415

Asn Leu Leu Gln Ala Asn Ala Gln Gln Asp Gly Lys Asp Tyr Ile Val
420 425 430

Leu Pro Ile Ser Glu Thr Leu Ser Met Glu Glu Asp Ser Gly Leu Ser
435 440 445

Leu Pro Thr Ser Pro Val Ser Cys Met Glu Glu Glu Val Cys Asp
450 455 460

Pro Lys Phe His Tyr Asp Asn Thr Ala Gly Ile Ser Gln Tyr Leu Gln
465 470 475 480

Asn Ser Lys Arg Lys Ser Arg Pro Val Ser Val Lys Thr Phe Glu Asp
485 490 495

Ile Pro Leu Glu Glu Pro Glu Val Lys Val Ile Pro Asp Asp Asn Gln
500 505 510

Thr Asp Ser Gly Met Val Leu Ala Ser Glu Glu Leu Lys Thr Leu Glu
515 520 525

Asp Arg Thr Lys Leu Ser Pro Ser Phe Gly Gly Met Val Pro Ser Lys
530 535 540

Ser Arg Glu Ser Val Ala Ser Glu Gly Ser Asn Gln Thr Ser Gly Tyr
545 550 555 560

Gln Ser Gly Tyr His Ser Asp Asp Thr Asp Thr Thr Val Tyr Ser Ser
565 570 575

Glu Glu Ala Glu Leu Leu Lys Leu Ile Glu Ile Gly Val Gln Thr Gly
580 585 590

Ser Thr Ala Gln Ile Leu Gln Pro Asp Ser Gly Thr Thr Leu Ser Ser
595 600 605

Pro Pro Val

610

<210> 26
<211> 1836
<212> DNA
<213> Homo Sapiens

<400> 1836

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ctacggaccg ttaagcccccaaatggaggg gaactgaaga caggctactt gtccatcgtc 180
atggatccag atgaactccc attggatgaa cattgtgaac gactgcctta tcatgcacgc 240
aaatggaaat tccccagaga cccggctgaag cttagtaagc ctcttgcccg tgggtgccttt 300
ggccaagtga ttgaagcaga tgcctttgga attgacaaga cagcaacttg caggacagta 360
gcagtcaaaa tggtaaaaga aggagcaaca cacagtggc atcgagctct catgtctgaa 420
ctcaagatcc tcattcatat tggtcaccat ctcaatgtgg tcaaccttct aggtgcctgt 480
accaagccag gagggccact catggtgatt gtggattct gcaaatttgg aaacctgtcc 540
acttacctga ggagcaagag aaatgaattt gtccccatac agaccaaagg ggcacgattc 600
cgtcaaggaa aagactacgt tggagcaatc cctgtggatc tgaaacggcg cttggacagc 660
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gtagaagaag aggaagctcc tgaagatctg tataaggact tcctgacctt ggagcatctc 780
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cacagggacc tggcgccacg aaatatcctc ttatcgaga agaacgtgg taaaatctgt 900
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cgccctccct tgaaatggat ggccccagaa acaatttttgc acagagtgtc cacaatccag 1020
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tatcctgggg taaagattga tgaagaattt tggatggcgat tgaaagaagg aactagaatg 1140
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